

US-09-323-5776-2.rq?

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OM protein - protein search, using sw model

Run on: May 8, 2001, 11:54:40 ; Search time 12.28 Seconds
(without alignments)
769,686 Million cell updates/sec

Title: US-09-323-5776-2
Sequence: 1 MALNSGSPPAIGPYENHGX.....YGVNVMYFTDMYRQMAADG 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues
Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCUTS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2717	100.0	492	4	US-09-342-749-2
2	1540	56.7	283	3	US-08-807-151-1
3	676.5	24.9	435	4	US-09-008-271A-6
4	660	24.3	798	1	US-08-200-900A-2
5	660	24.3	798	5	PCR-US94-00616-2
6	558.5	20.6	855	2	US-09-027-337-2
7	356	19.9	638	2	US-08-681-151-3
8	539.5	19.7	416	2	US-09-000-846-2
9	534	19.9	356	2	US-08-681-151-1
10	528.5	19.5	256	2	US-09-027-337-3
11	527.5	19.4	418	1	US-08-508-446C-25
12	521.5	19.2	235	3	US-08-807-151-3
13	518.5	19.1	812	1	US-08-248-629A-1
14	518.5	19.1	812	1	US-08-451-932-1
15	518.5	19.1	812	1	US-08-452-260-1
16	518.5	19.1	812	1	US-08-326-785-1
17	518.5	19.1	812	2	US-08-612-788-1
18	518.5	19.1	812	2	US-08-603-598B-1
19	518.5	19.1	812	2	US-08-429-743-1
20	518.5	19.1	812	2	US-08-866-735-1
21	518.5	19.1	812	3	US-09-066-028-1
22	518.5	19.1	812	5	PCR-US95-05107-1
23	513.5	18.9	232	4	US-08-508-446C-19
24	459.5	16.9	314	4	US-09-008-271A-3
25	450	16.6	546	6	5200340-6
26	450	16.6	270	4	US-08-978-404B-8
27	449	16.5	655	1	US-08-148-910-12

28	449	16.5	655	1	US-08-448-937A-12	Sequence 12, Appl
29	447	16.5	276	2	US-09-016-366A-15	Sequence 15, Appl
30	447	16.5	276	2	US-08-978-404B-21	Sequence 21, Appl
31	446	16.4	230	1	US-08-379-621-2	Sequence 2, Appl1
32	446	16.4	230	1	US-08-147-000B-2	Sequence 2, Appl1
33	446	16.4	230	2	US-08-889-078-2	Sequence 2, Appl1
34	445.5	16.4	791	1	US-08-643-219-1	Sequence 1, Appl1
35	445.5	16.4	791	2	US-09-131-995-1	Sequence 1, Appl1
36	445.5	16.4	791	2	US-08-832-087B-1	Sequence 1, Appl1
37	445.5	16.4	791	3	US-08-851-350-1	Sequence 1, Appl1
38	445.5	16.4	810	1	US-07-854-603-2	Sequence 1, Appl1
39	445.5	16.4	810	1	US-08-147-000B-29	Sequence 29, Appl
40	445.5	16.4	810	6	5200340-8	Patent No. 5200340
41	444.5	16.4	790	1	US-08-469-486-54	Sequence 54, Appl
42	444.5	16.4	790	2	US-08-469-658-54	Sequence 54, Appl
43	442.5	16.3	222	1	US-08-456-840-46	Sequence 46, Appl
44	442.5	16.3	222	1	US-08-266-407A-46	Sequence 46, Appl
45	442.5	16.3	222	2	US-08-892-544-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1									
US-09-342-749-2									
Sequence 2, Application US/09342749									
Patent No. 6166194									
GENERAL INFORMATION:									
APPLICANT: Wong, Alexander K.C.									
APPLICANT: Tavligian, Sean V.									
APPLICANT: Teng, David H.-F.									
APPLICANT: Myriad Genetics, Inc.									
TITLE OF INVENTION: TMRSS2 is a Tumor Suppressor									
FILE REFERENCE: 2318-202									
CURRENT APPLICATION NUMBER: US/09/342,749									
CURRENT FILING DATE: 1999-06-29									
EARLIER APPLICATION NUMBER: US 60/091,044									
NUMBER OF SEQ ID NOS: 33									
SOFTWARE: PatentIn Ver. 2.0									
SEQ ID NO 2									
LENGTH: 492									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-09-342-749-2									
Query Match									
Best Local Similarity 100.0%; Score 2717; DB 4; Length 492;									
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MALNSGSPPAIGPYENHGX	OPENPYPAQTV	PYVEVHPA	QYVPP	POYAPR	LVLOA	60	
DB	1	MALNSGSPPAIGPYENHGX	OPENPYPAQTV	PYVEVHPA	QYVPP	POYAPR	LVLOA	60	
QY	61	SNPVCTOPKSPSGVCTSKTKAL	CTLTTLT	FLVGA	LAAGL	LMKFGS	KCSNSG	IEC	120
DB	61	SNPVCTOPKSPSGVCTSKTKAL	CTLTTLT	FLVGA	LAAGL	LMKFGS	KCSNSG	IEC	120
QY	121	DSSGTCINSNMC	DGVS	HRPG	GEDE	RCVRL	GP	PILOV	YS
DB	121	DSSGTCINSNMC	DGVS	HRPG	GEDE	RCVRL	GP	PILOV	YS
QY	181	GRACRDMKYNKFYS	SSQIG	IVD	SGTSP	KMT	SAG	NDV	IKKLYHSD
DB	181	GRACRDMKYNKFYS	SSQIG	IVD	SGTSP	KMT	SAG	NDV	IKKLYHSD
QY	241	CIACGVNLSS	RQSR	IVG	GESAL	PGAMP	QVSL	AVON	HVCGS
DB	241	CIACGVNLSS	RQSR	IVG	GESAL	PGAMP	QVSL	AVON	HVCGS
QY	301	PLNNPMHWA	FGTIL	RQSN	ME	GAG	QV	EVK	YS
DB	301	PLNNPMHWA	FGTIL	RQSN	ME	GAG	QV	EVK	YS

Db 301 PLNNPMTAFAGILROSFMFYGAGYOVEKIVSHPNIDSKTKNDIALMKLQPLTFNDL 360
Qy 361 VKPYCLPNPGLMLOPEQLCWSISGNGATEEKGKTSVLLNAKVLIIETORNSRYVDNLI 420
Db 361 VKPYCLPNPGLMLOPEQLCWSISGNGATEEKGKTSVLLNAKVLIIETORNSRYVDNLI 420
Qy 421 TPAMICAGFLAGNDSCGDSGGPLVTSKNNIMWLIDTSMGSCAKAYRPGYGNMVF 480
Db 421 TPAMICAGFLAGNDSCGDSGGPLVTSKNNIMWLIDTSMGSCAKAYRPGYGNMVF 480
Qy 481 TDMYRQMRADG 492
Db 481 TDMYRQMRADG 492

RESULT 2

US-08-807-151-1
; Sequence 1, Application US/08807151
; Patent No. 6043033
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED
; TITLE OF INVENTION: PROTEASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/807,151
; FILING DATE: Filed Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SCORNO701
; CLONE: 556016
; US-08-807-151-1

Query Match 56.7%; Score 1540; DB 3; Length 283;
Local Similarity 99.6%; Pred. No. 1.3e-133;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 56.7%; Score 1540; DB 3; Length 283;
Local Similarity 99.6%; Pred. No. 1.3e-133;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 61 QVSLHVNQNVHCGGSIITPEWITAAHCVEKPLNPNMHTAFAGILROSFMFYGAGYOVE 120
Qy 330 KVISHPNYSKTKNDIALMKLQPLTFNDLVKPYCLPNPGLMLOPEQLCWSISGNGATEE 389
Db 121 KVISHPNYSKTKNDIALMKLQPLTFNDLVKPYCLPNPGLMLOPEQLCWSISGNGATEE 180
Qy 390 KGTSEVLLNAKAVLLIETORNSRYVDNLIPTAMICAGFLAGNDSCGDSGGPLVTSK 449
Db 181 KGTSEVLLNAKAVLLIETORNSRYVDNLIPTAMICAGFLAGNDSCGDSGGPLVTSK 240
Qy 450 NNTIMWLIDTSMGSCAKAYRPGYGNMVFETDMYRQMRADG 492
Db 241 NNTIMWLIDTSMGSCAKAYRPGYGNMVFETDMYRQMRADG 283

RESULT 3

US-09-008-271A-6
; Sequence 6, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Tom Y.
; APPLICANT: Shah, Puryl
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheila
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNNO713
; CLONE: 1337018
; SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

US-09-008-271A-6

Query Match 24.9%; Score 676.5; DB 4; Length 435;
Best Local Similarity 39.1%; Pred. No. 4.8e-54;
Matches 150; Conservative 57; Mismatches 128; Indels 49; Gaps 13;

Query Match 24.9%; Score 676.5; DB 4; Length 435;
Best Local Similarity 39.1%; Pred. No. 4.8e-54;
Matches 150; Conservative 57; Mismatches 128; Indels 49; Gaps 13;